

Figure 2

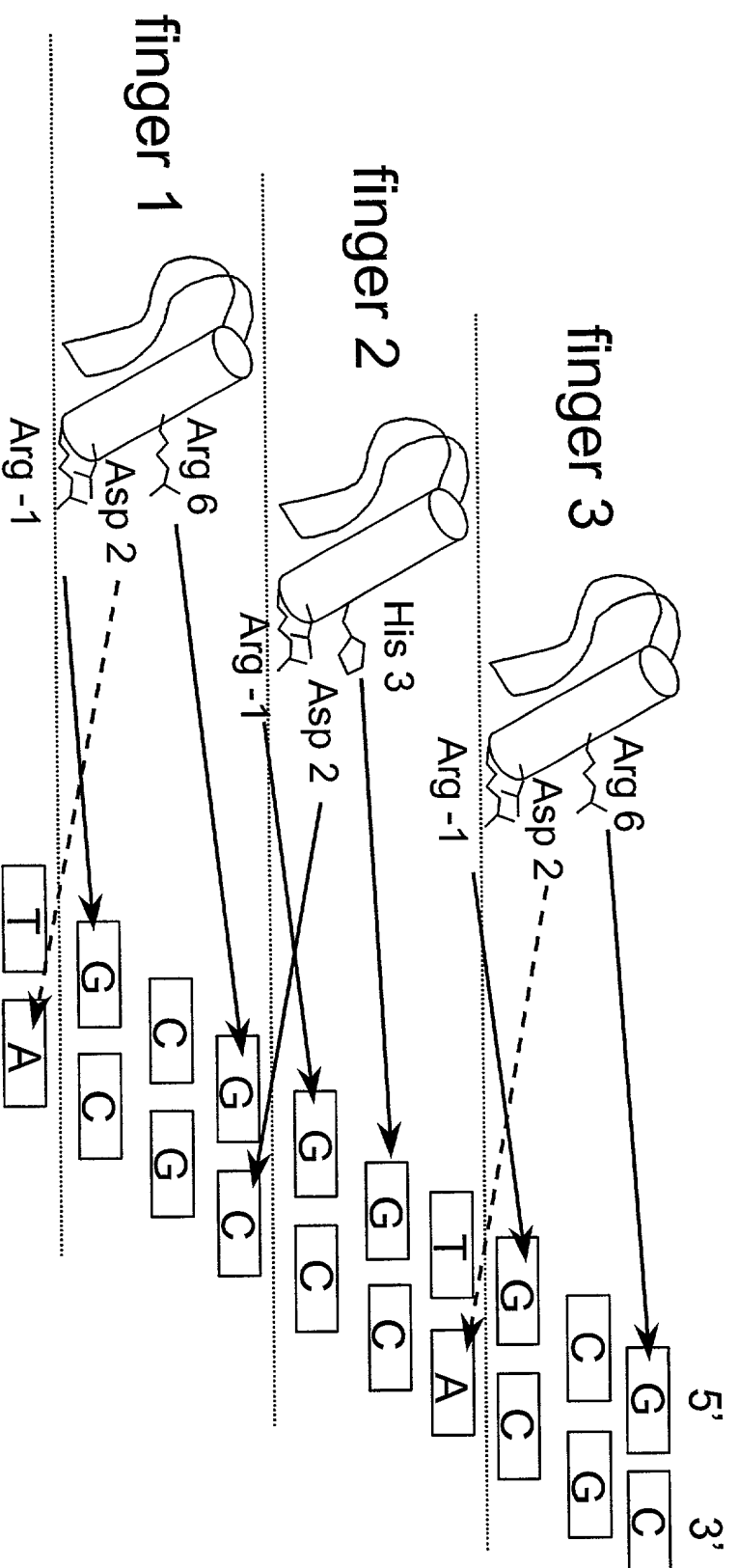
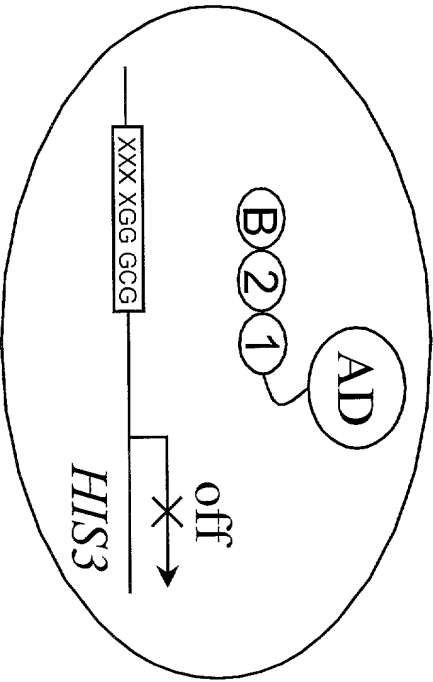
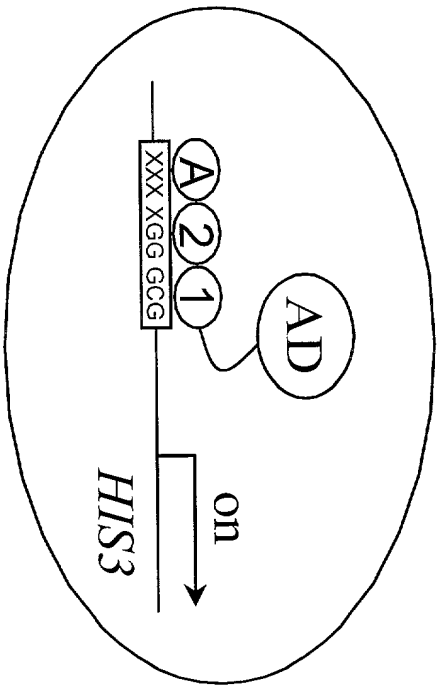


Figure 3

Base				
	G	A	C	T
Position in triplet	Arg6 Lys6 Asp2 Ser2	Gln6	Ser2	Lys6 Asp2
	His3 Lys3	Asn3 Ser3 His3	Asp3 Thr3 Val3 Leu3	Thr3 Ala3 Ser3 Val3
	Arg-1	Gln-1	Asp-1	Leu-1 Thr-1 Asn-1

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Figure 5



Growth on

Yes

No

— histidine plates

Figure 6

HIV-1 LTR (-124/-115):	5'-GAC ATC <u>GAG C</u> -3'	(SEQ ID NO:1)
HIV-1 LTR (-23/-14):	5'-GCA GCT <u>GCT T</u> -3'	(SEQ ID NO:2)
HIV-1 LTR (-95/-86):	5'-GCT GGG <u>GAC T</u> -3'	(SEQ ID NO:3)
Human CCR5 (-70/-79):	5'-AGG GTG <u>GAG T</u> -3'	(SEQ ID NO:4)
Human CCR5 (+7/+16):	5'-GCT GAG <u>ACA T</u> -3'	(SEQ ID NO:5)

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Figure 7

GCGT (optimal Zif268-binding site)

5'-CCG GCGTGGGCG GCT GCGTGGGCG T GCGTGGGCG GACT GCGTGGGCG-3' (SEQ ID NO:6)
3'-GCACCCGC CGA CGCACCCGC A CGCACCCGC CTGA CGCACCCGC AGCT-5' (SEQ ID NO:7)

GAGC (HIV-1 LTR, -118/-115)

5'-CCGGC GAGCGGGCG GTC GAGCGGGCG T GAGCGGGCG GATC GAGCGGGCG-3' (SEQ ID NO:8)
3'-G CTCGCCCCG CAG CTCGCCCCG A CTCGCCCCG CTAG CTCGCCCCG AGCT-5' (SEQ ID NO:9)

GCTT (HIV-1 LTR, -17/-14)

5'-CCGGCT GCTTGGGCG GCT GCTTGGGCG T GCTTGGGCG GGCT GCTTGGGCG-3' (SEQ ID NO:10)
3'-GA CGAACCCGC CGA CGAACCCGC A CGAACCCGC CCGA CGAACCCGC AGCT-5' (SEQ ID NO:11)

GACT (HIV-1 LTR, -89/-86)

5'-CCG GACTGGGCG GGG GACTGGGCG T GACTGGGCG GAGG GACTGGGCG-3' (SEQ ID NO:12)
3'-TGACCCGC CCC CTGACCCGC A CTGACCCGC CTCC CTGACCCGC AGCT-5' (SEQ ID NO:13)

GAGT (Human CCR5, -76/-79)

5'-CCG GAGTGGGCG GTG GAGTGGGCG T GAGTGGGCG GATG GAGTGGGCG-3' (SEQ ID NO:14)
3'-TCACCCGC CAC CTCACCCGC A CTCACCCGC CTAC CTCACCCGC AGCT-5' (SEQ ID NO:15)

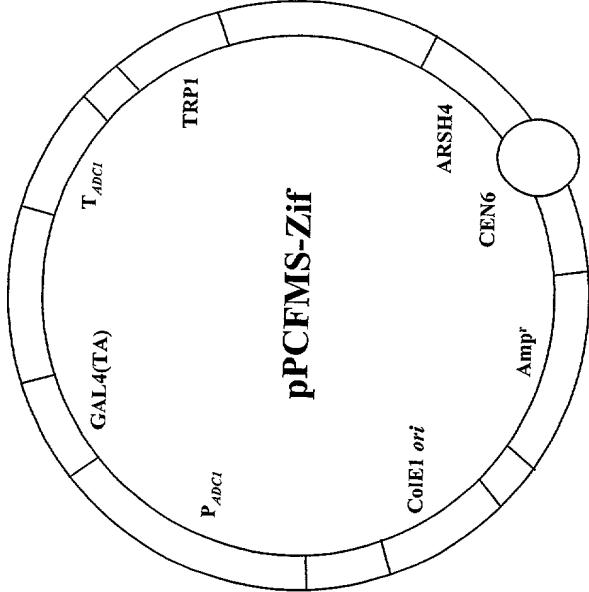
ACAT (Human CCR5, +13/+16)

5'-CCGG ACATGGGCG GAG ACATGGGCG T ACATGGGCG GAAG ACATGGGCG-3' (SEQ ID NO:16)
3'-TGTACCCGC CTC TGTACCCGC A TGTACCCGC CTC TGTACCCGC AGCT-5' (SEQ ID NO:17)

Figure 8

5'-GAG-3' (top strand)
3'-CTC-5' (bottom strand)

Lys	Glu	Gly	Gly	Ser	Thr	Phe	Arg	Thr	Gly	Gln	Glu	Arg	Pro	Zif268	Asp	Pro	Arg	Glu			
AAA	CAG	GGT	GGG	TCG	ACC	TTC	CGG	ACT	GGC	CAG	GAA	CGC	CCA	---	---	GAT	CCG	CGG	GAA		
Sali															EcoRI						
Phe Arg Ser Thr Ser Ala Ala Ala Lys Stop																					
TTC	AGA	TCT	ACT	AGT	<u>GCG</u>	GCC	GCT	ATG	TAA	GTA	AGA	CGT	CGA	<u>GCT</u>	CGC	CAT	CGC	GST	GGA	AGC	TTT
NotI										SacI											



Zif268

Finger 1	Finger 2	Finger 3
BspEI/MscI	MscI	BspEI/SgrAI
		SacII

GGG TCG ACC TTC CGG ACT GGC CAG GAA CGC CCA TAT GCT TGC CCT GTC GAG TCC TGC
SalI *BspEI* *MscI*

Q K P F Q C R I C M R N F S R S D H L
CAG AAG CCC TTC CAG TGT CGA ATC TGC ATG CGT AAC TTC AGT CGT AGT GAC CAC CTT

R K F A R S D E R K R H T K I H L R Q
AGG AAG TTT GCC AGG AGT GAT GAA CGC AAG AGG CAT ACC AAA ATC CAT TTA AGA CAG

K D (SEQ ID NO: 21)
AAG GAT CCG CGG GAA TCC (SEQ ID NO: 20)
SacII EcoRI

Figure 10

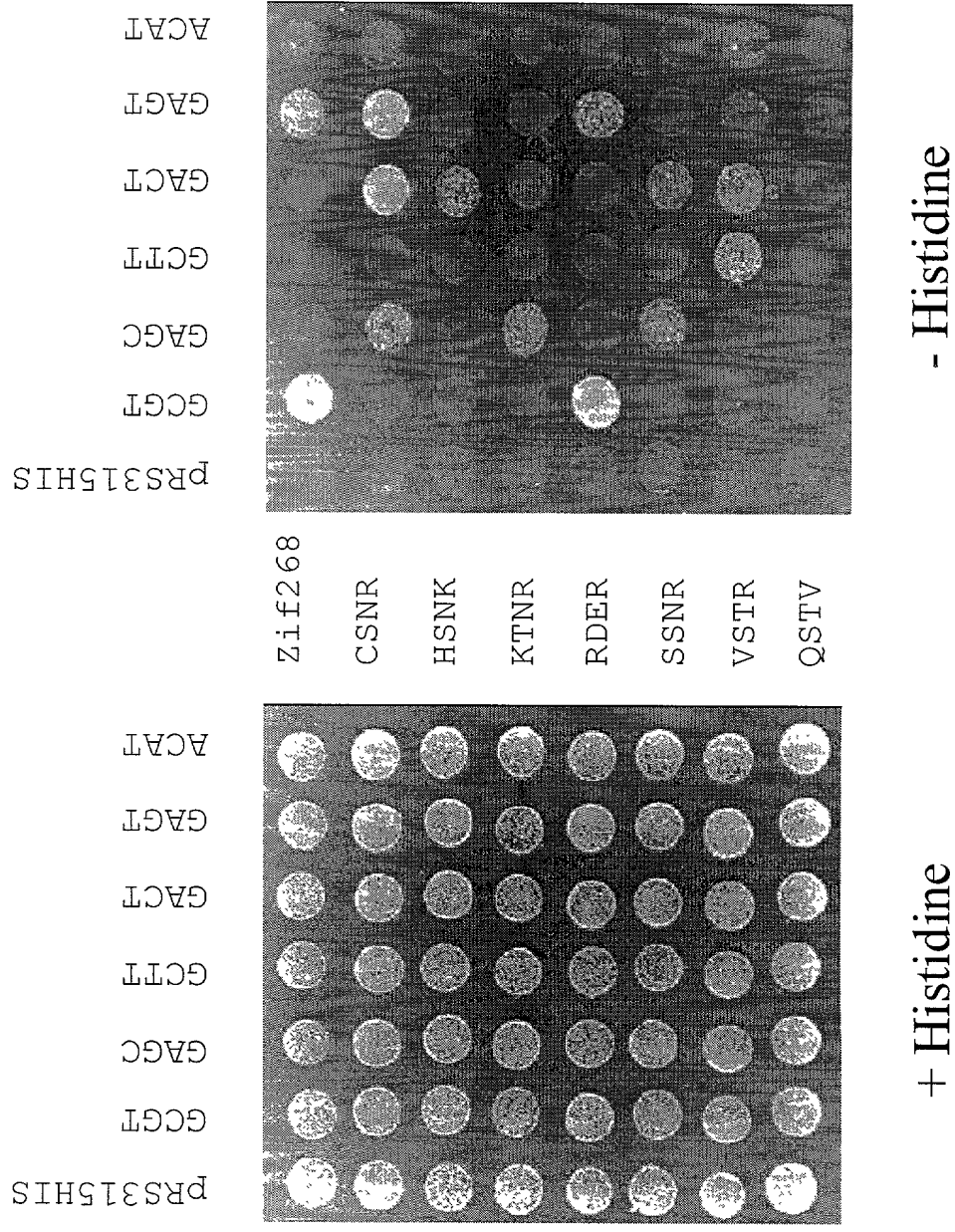


Figure 11

CSNR:

T G Q K P Y K C K Q C G K A F G C P S
ACC GGG CAG AAA CCG TAC AAA TGT AAG CAA TGT GGG AAA GCT TTT GGA TGT CCC TCA
 N L R R H G R T H T G E K P R (SEQ ID NO:23)
 AAC CTT CGA AGG CAT GGA AGG ACT CAC ACC GGC GAG AAA CCG CGG (SEQ ID NO:22)
 3 6 -1 2

HSNK:

T G E K P Y K C K E C G K A F N H S S
ACC GGG GAG AAG CCA TAC AAG TGT AAG GAG TGT GGG AAA GCC TTC AAC CAC AGC TCC
 N F N K H H R I H T G E K P R (SEQ ID NO:25)
 AAC TTC AAT AAA CAC CAC AGA ATC CAC ACC GGC GAA AAG CCG CGG (SEQ ID NO:24)
 3 6 -1 2

SSNR:

T G E R P F E C K E C G K A F S S G S
ACC GGG GAG AGG CCA TTT GAA TGT AAG GAA TGT GGG AAA GCC TTT AGT AGT GGT TCA
 N F T R H Q R I H T G E K P R (SEQ ID NO:27)
 AAC TTC ACT CGA CAT CAG AGA ATT CAC ACC GGT GAA AAG CCG CGG (SEQ ID NO:26)
 3 6 -1 2

RDER:

T G Q K P Y V C D V E G C T W K F A R
ACC GGG CAG AAG CCA TAC GTA TGC GAT GTA GAG GGA TGT ACG TGG AAA TTT GCC CGC
 S D E L N R H K K R H T G E R P R (SEQ ID NO:29)
 TCA GAT GAG CTC AAC AGA CAC AAG AAA AGG CAC ACC GGC GAA AGA CCG CGG (SEQ ID NO:28)
 2 3 6 -1

QSTV:

T G E R P Y E C N E C G K A F A Q N S
ACC GGG GAG AGA CCT TAC GAG TGT AAT GAA TGC GGG AAA GCT TTT GCC CAA AAT TCA
 T L R V H Q R I H T G E K P R (SEQ ID NO:31)
 ACT CTC AGA GTA CAC CAG AGA ATT CAC ACC GGC GAA AAG CCG CGG (SEQ ID NO:30)
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VSTR:

T G E R P Y E C N Y C G K T F S V S S
ACC GGG GAG AGG CCT TAT GAG TGT AAT TAC TGT GGA AAA ACC TTT AGT GTG AGC TCA
 T L I R H Q R I H T G E R P R (SEQ ID NO:33)
 ACC CTT ATT AGA CAT CAG AGA ATC CAC ACC GGC GAG AGA CCG CGG (SEQ ID NO:32)
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